Amendments to the specification

Please replace the entire paragraph at page 1, lines 5-21, with the following amended paragraph:

This application (the "instant application") ~~claims the benefit of~~ is a continuation-in-part of prior U.S. Application No. 10/412,699, filed April 10, 2003 (pending), which is a continuation-in-part of prior ~~in turn claims the benefit of~~ U.S. ~~Non-provisional~~ Application No. 09/533,030, filed March 22, 2000 (abandoned), ~~which in turn claims the benefit of U.S. Provisional Application No. 60/125,814, filed March 23, 1999~~; prior U.S. Application 10/171,468, filed June 14, 2002 (abandoned), and prior U.S. ~~Non-provisional~~ Application No. 09/713,994, filed November 16, 2000 (pending) which claims the benefit of U.S. Provisional Application No. 60/166,228, filed November 17, 1999; and, the instant application is a continuation-in-part of prior U.S. Application No. 09/713,994, filed November 16, 2000 (pending), which ~~in turn~~ claims the benefit of U.S. Provisional Application No. 60/166,228, filed November 17, 1999 (abandoned); ~~U.S. Provisional Application No. 60/197,899, filed April 17, 2000, and U.S. Provisional Application No. 60/227,439, filed August 22, 2000~~; and, the instant application is a continuation-in-part of prior U.S. ~~Non-provisional~~ Application No. 10/112,887, filed March 18, 2002 (pending); and, the instant application is a continuation-in-part of prior U.S. ~~Non-provisional~~ Application No. 10/286,264, filed ~~January 23, 2003~~ (pending), which is a divisional application of prior U.S. Application No. 09/533,030, filed March 22, 2000 (abandoned), which in turn claims the benefit of prior U.S. Provisional Application No. 60/125,814, filed March 23, 1999 (abandoned); and, the instant application is a continuation-in-part of prior U.S. ~~Non-provisional~~ Application No. 10/225,068, filed August 9, 2002 (pending), which is a continuation-in-part of prior U.S. Application No. 10/171,468, filed June 14, 2002 (abandoned), which is a continuation-in-part of prior U.S. Application No. 09/837,944, filed April 18, 2001 (abandoned), and U.S. Application No. 10/225,068 claims the benefit of U.S. Provisional Application No. 60/310,847, filed August 9, 2001 (abandoned) and U.S. Provisional Application No. 60/336,049, filed November 19, 2001 (abandoned); and, the instant application is a continuation-in-part of prior U.S. ~~Non-provisional~~ Application No. 10/225,066, filed August 9, 2002 (pending), which claims the benefit of U.S. Provisional Application No. 60/336,049, filed November 19, 2001 (abandoned); and, the instant application is a continuation-in-part of prior U.S. ~~Non-provisional~~ Application No. 10/374,780, filed February 25, 2003 (pending), which ~~claims the benefit~~ is a continuation-in-part of prior U.S. ~~Non-provisional~~ Application No. 09/837,944, filed April 18, 2001 (abandoned), ~~U.S. Non-provisional Application No. 10/171,468, filed June 14, 2002, U.S.~~

~~Provisional Application No. 60/310,847, filed August 9, 2001, and U.S. Provisional Application No. 60/336,049, filed November 19, 2001~~; and, the instant application is a continuation-in-part of prior U.S. ~~Non-provisional~~ Application ~~"Polynucleotides and Polypeptides in Plants"~~ No. 10/666,642, filed September 18, 2003 (pending), which claims the benefit of U.S. Provisional Application No. 60/434,166, filed December 17, 2002 (pending), and U.S. Provisional Application No. 60/411,837, filed September 18, 2002 (abandoned). The entire contents of all of these applications are hereby incorporated by reference.

Please replace the paragraph at page 12, line 8-17 with the following amended paragraph (in line 12, delete "of" after "downstream)":

Operationally, genes may be defined by the cis-trans test, a genetic test that determines whether two mutations occur in the same gene and that may be used to determine the limits of the genetically active unit (Rieger et al. (1976) Glossary of Genetics and Cytogenetics: Classical and Molecular, 4th ed., Springer Verlag, Berlin). A gene generally includes regions preceding ("leaders"; upstream) and following ("trailers"; downstream) [[of]] the coding region. A gene may also include intervening, non-coding sequences, referred to as "introns", located between individual coding segments, referred to as "exons". Most genes have an associated promoter region, a regulatory sequence 5' of the transcription initiation codon (there are some genes that do not have an identifiable promoter). The function of a gene may also be regulated by enhancers, operators, and other regulatory elements.

Please replace the paragraph at page 16, line 32 to page 17, line 1 with the following amended paragraph:

With regard to polynucleotide variants, differences between presently disclosed polynucleotides and polynucleotide variants are limited so that the nucleotide sequences of the former and the latter are closely similar overall and, in many regions, identical. Due to the degeneracy of the genetic code, differences between the former and latter nucleotide sequences [[o]] may be silent (i.e., the amino acids encoded by the polynucleotide are the same, and the variant polynucleotide sequence encodes the same amino acid sequence as the presently disclosed polynucleotide. Variant nucleotide sequences may encode different amino acid sequences, in which case such nucleotide differences will result in amino acid substitutions, additions,

deletions, insertions, truncations or fusions with respect to the similar disclosed polynucleotide sequences. These variations result in polynucleotide variants encoding polypeptides that share at least one functional characteristic. The degeneracy of the genetic code also dictates that many different variant polynucleotides can encode identical and/or substantially similar polypeptides in addition to those sequences illustrated in the Sequence Listing.

Please replace the paragraph at page 19, line 32 through page 20, line 7 with the following amended paragraph:

"Fragment", with respect to a polynucleotide, refers to a clone or any part of a polynucleotide molecule that retains a usable, functional characteristic. Useful fragments include oligonucleotides and polynucleotides that may be used in hybridization or amplification technologies or in the regulation of replication, transcription or translation. A "polynucleotide fragment" refers to any subsequence of a polynucleotide, typically, of at least about 9 consecutive nucleotides, preferably at least about 30 nucleotides, more preferably at least about 50 nucleotides, of any of the sequences provided herein. Exemplary polynucleotide fragments are the first sixty consecutive nucleotides of the transcription factor polynucleotides listed in the Sequence Listing. Exemplary fragments also include fragments that comprise a region that encodes a B domain of a transcription factor, for example, amino acid residues 26-116 of G482 (SEQ ID NO: 4), as noted in Table 1.

Please replace the entire paragraph at page 72, line 17 - 29 with the following amended paragraph:

Vectors expressing an untranslatable form of the transcription factor mRNA, e.g., sequences comprising one or more stop codon, or nonsense mutation) can also be used to suppress expression of an endogenous transcription factor, thereby reducing or eliminating its activity and modifying one or more traits. Methods for producing such constructs are described in US Patent No. 5,583,021. Preferably, such constructs are made by introducing a premature stop codon into the transcription factor gene. Alternatively, a plant trait can be modified by gene silencing using double-stranded RNA (Sharp (1999) *Genes and Development* 13: 139-141). Another method for abolishing the expression of a gene is by insertion mutagenesis using the T-

DNA of *Agrobacterium tumefaciens*. After generating the insertion mutants, the mutants can be screened to identify those containing the insertion in a transcription factor or transcription factor homolog gene. Plants containing a single transgene insertion event at the desired gene can be crossed to generate homozygous plants for the mutation. Such methods are well known to those of skill in the art (See for example Koncz et al. (1992) Methods in *Arabidopsis* Research, World Scientific Publishing Co. Pte. Ltd., River Edge, NJ).

Please replace the entire paragraph at page 71, line 27 through page 72, line 16 with the following amended paragraph:

Suppression of endogenous transcription factor gene expression can also be achieved using RNA interference (RNAi) or microRNA-based methods (Llave et al. (2002) *Science* 297: 2053-2056; Tang et al. (2003) *Genes Dev.* 17: 49-63). RNAi is a post-transcriptional, targeted gene-silencing technique that uses double-stranded RNA (dsRNA) to incite degradation of messenger RNA (mRNA) containing the same sequence as the dsRNA (Constans, (2002) *The Scientist* 16: 36). Small interfering RNAs, or siRNAs are produced in at least two steps: an endogenous ribonuclease cleaves longer dsRNA into shorter, 21-23 nucleotide-long RNAs (Plasterk (2002) *Science* 296: 1263-1265). The siRNA segments then mediate the degradation of the target mRNA (Zamore, (2001) *Nature Struct. Biol.*, 8:746-50). RNAi has been used for gene function determination in a manner similar to antisense oligonucleotides (Constans, (2002) *The Scientist* 16:36). Expression vectors that continually express siRNAs in transiently and stably transfected cells have been engineered to express small hairpin RNAs (shRNAs), which get processed in vivo into siRNAs-like molecules capable of carrying out gene-specific silencing (Brummelkamp et al., (2002) *Science* 296:550-553, and Paddison, et al. (2002) *Genes & Dev.* 16:948-958). Post-transcriptional gene silencing by double-stranded RNA is discussed in further detail by Hammond et al. (2001) *Nature Rev Gen* 2: 110-119, Fire et al. (1998) *Nature* 391: 806-811 and Timmons and Fire (1998) *Nature* 395: 854. Vectors in which RNA encoded by a transcription factor or transcription factor homolog cDNA is over-expressed can also be used to obtain co-suppression of a corresponding endogenous gene, e.g., in the manner described in US Patent No. 5,231,020 to Jorgensen. Such co-suppression (also termed sense suppression) does not require that the entire transcription factor cDNA be introduced into the plant cells, nor does it require that the introduced sequence be exactly identical to the endogenous transcription factor gene of interest. However, as with antisense suppression, the suppressive efficiency will be

enhanced as specificity of hybridization is increased, e.g., as the introduced sequence is lengthened, and/or as the sequence similarity between the introduced sequence and the endogenous transcription factor gene is increased.

Please replace the entire paragraph at page 73, lines 24 - 31 with the following amended paragraph

The plant can be any higher plant, including gymnosperms, monocotyledonous and ~~dicotyledenous~~ dicotyledonous plants. Suitable protocols are available for *Leguminosae* (alfalfa, soybean, clover, etc.), *Umbelliferae* (carrot, celery, parsnip), *Cruciferae* (cabbage, radish, rapeseed, broccoli, etc.), *Curcurbitaceae* (melons and cucumber), *Gramineae* (wheat, corn, rice, barley, millet, etc.), *Solanaceae* (potato, tomato, tobacco, peppers, etc.), and various other crops. See protocols described in Ammirato et al., eds., (1984) Handbook of Plant Cell Culture –Crop Species, Macmillan Publ. Co., New York, NY; Shimamoto et al. (1989) *Nature* 338: 274-276; Fromm et al. (1990) *Bio/Technol.* 8: 833-839; and Vasil et al. (1990) *Bio/Technol.* 8: 429-434.

Please replace the entire paragraph at page 88, lines 10-15 with the following amended paragraph:

Stress assays that were conducted with more mature plants also included high salt stress (6 hour exposure to 200 mM NaCl), drought stress (168 hours after removing water from trays), osmotic stress (6 hour exposure to 3 M mannitol), or nutrient limitation (nitrogen, phosphate, and potassium) (nitrogen: all components of MS medium remained constant except N was reduced to 20 mg/l of NH_4NO_3; phosphate: all components of MS medium except ~~$KH2PO_4$~~ KH_2PO_4, which was replaced by K_2SO_4; potassium: all components of MS medium except removal of KNO_3 and KH_2PO_4, which were replaced by NaH_4PO_4).

Please replace the entire paragraph at page 88, line 32 through page 89, line 3 with the following amended paragraph (in line 1 on page 89, after "concentration", delete "of"):

Salt stress assays are intended to find genes that confer better germination, seedling vigor or growth in high salt. Evaporation from the soil surface causes upward water movement and salt accumulation in the upper soil layer where the seeds are placed. Thus, germination normally takes

place at a salt concentration much higher than the mean salt concentration [[of]] in the whole soil profile. Plants differ in their tolerance to NaCl depending on their stage of development, therefore seed germination, seedling vigor, and plant growth responses are evaluated.

Please delete the following paragraphs at page 89, lines 21 -34:

~~Germination assays followed modifications of the same basic protocol. Sterile seeds were sown on the conditional media listed below. Plates were incubated at 22° C under 24 hour light (120-130 μEin/m²/s) in a growth chamber. Evaluation of germination and seedling vigor was conducted 3 to 15 days after planting. The basal media was 80% Murashige-Skoog medium (MS) + vitamins.~~

~~For salt and osmotic stress germination experiments, the medium was supplemented with 150 mM NaCl or 300 mM mannitol. Growth regulator sensitivity assays were performed in MS media, vitamins, and either 0.3 μM ABA, 9.4% sucrose, or 5% glucose.~~

~~Temperature stress cold germination experiments were carried out at 8 °C. Heat stress germination experiments were conducted at 32 °C to 37° C for 6 hours of exposure.~~

~~For stress experiments conducted with more mature plants, seeds were germinated and grown for seven days on MS + vitamins + 1% sucrose at 22 °C and then transferred to chilling and heat stress conditions. The plants were either exposed to chilling stress (6 hour exposure to 4-8° C), or heat stress (32° C was applied for five days, after which the plants were transferred back 22 °C for recovery and evaluated after 5 days relative to controls not exposed to the depressed or elevated temperature).~~

Please replace the entire paragraph at page 97, line 24 through page 98, line 1 with the following amended paragraph:

The "one-hybrid" strategy (Li and Herskowitz (1993) *Science* 262: 1870-1874) is used to screen for plant cDNA clones encoding a polypeptide comprising a transcription factor DNA binding domain, a conserved domain. In brief, yeast strains are constructed that contain a lacZ reporter gene with either wild-type or mutant transcription factor binding promoter element sequences in place of the normal UAS (upstream activator sequence) of the ~~GALL~~GAL4 promoter. Yeast reporter strains are constructed that carry transcription factor binding promoter element sequences as UAS elements are operably linked upstream (5') of a lacZ reporter gene

with a minimal ~~GAL1~~GAL4 promoter. The strains are transformed with a plant expression library that contains random cDNA inserts fused to the GAL4 activation domain (GAL4-ACT) and screened for blue colony formation on X-gal-treated filters (X-gal: 5-bromo-4-chloro-3-indolyl-β-D-galactoside; Invitrogen Corporation, Carlsbad CA). Alternatively, the strains are transformed with a cDNA polynucleotide encoding a known transcription factor DNA binding domain polypeptide sequence.

Please replace the entire paragraph at page 103, lines 8 - 11 with the following amended paragraph:

Similarly, the amino acid sequences of the three CBF polypeptides range from 84 to 86% identity. An alignment of the three amino acid[[ic]] sequences reveals that most of the differences in amino acid sequence occur in the acidic C-terminal half of the polypeptide. This region of CBF1 serves as an activation domain in both yeast and *Arabidopsis* (not shown).

Please replace the entire Table 6 at page 95, line 1 with the following amended table.

Table 6. Summary of Results of Physiological Assays.

GID	Polynucleotide SEQ ID NO	Promoter	[illegible]	Overexpressor lines showing phenotype: [illegible]	[illegible]	[illegible]	[illegible]	[illegible]	[illegible]
G482	[[2]] 4	CaMV 35S	2-components-supTfn	+			+*		
		CaMV 35S	Direct promoter-fusion			+			
G481	[[4]] 2	CaMV 35S	Direct promoter-fusion		+		++**		
		ARSK1	2-components-supTfn						++
		CaMV 35S	Superactivation			+			
		CaMV 35S	RNAi (GS)	++	+		+**		
G485	6	CaMV 35S	2-components-supTfn			+	+**	+	+
G3395	74	CaMV 35S	Direct promoter-fusion			+			

* Mannitol ** Sucrose

Abbreviations: Sens. Sensitivity
Germ. Germination

\+ Moderate trait manifestation in one or more lines tested
++ Strong trait manifestation in one or more lines tested